60

CGGGGAGGAATATGCTGTGGAGCTCCTCTGCCATATAAACAAAAAGAGGAAATCTTTCAA 60 ACATGGCTGAAGCAAAGACCCACTGGCTTGGAGCAGCCCTGTCTCTTATCCCTTTAATTT 120 5 CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG 240 AGTACATAGAAAACCCCTTTAAACGCACAAATGAAATAGTGGAGGAACAATATACTCCTC 300 AAAGCCTTGCTACATTGGAATCTGTCTTCCAAGAGCTGGGGAAACTGACAGGACCAAACA 360 ACCAGAAACGTGAGAGGATGGATGAGGAGCAAAAACTTTATACGGATGATGAAGATGATA 420 TCTACAAGGCTAATAACATTGCCTATGAAGATGTGGTCGGGGGAGAAGACTGGAACCCAG 480 10 TAGAGGAGAAAATAGAGAGTCAAACCCAGGAAGAGGTGAGAGACAGCAAAGAGAATATAG 540 GAAAAAATGAACAAATCAACGATGAGATGAAACGCTCAGGGCAGCTTGGCATCCAGGAAG 600 AAGATCTTCGGAAAGAGAGTAAAGACCAACTCTCAGATGATGTCTCCAAAGTAATTGCCT 660 ATTTGAAAAGGTTAGTAAATGCTGCAGGAAGTGGGAGGTTACAGAATGGGCAAAATGGGG 720 AAAGGGCCACCAGGCTTTTTGAGAAACCTCTTGATTCTCAGTCTATTTATCAGCTGATTG 780 15 AAATCTCAAGGAATTTACAGATACCCCCAGAAGACTTAATTGAGATGCTCAAAACTGGGG 840 AGAAGCCGAATGGATCAGTGGAACCGGAGCGGGAGCTTGACCTTCCTGTTGACCTAGATG 900 ACATCTCAGAGGCTGACTTAGACCATCCAGACCTGTTCCAAAATAGGATGCTCTCCAAGA 960 GTGGCTACCCTAAAACACCTGGTCGTGCTGGGACTGAGGCCCTACCAGACGGGCTCAGTG 1020 TTGAGGATATTTTAAATCTTTTAGGGATGGAGAGTGCAGCAAATCAGAAAACGTCGTATT 1080 20 TTCCCAATCCATATAACCAGGAGAAAGTTCTGCCAAGGCTCCCTTATGGTGCTGGAAGAT 1140 CATATGAAAACCTGAACGACAAGGATCAAGAATTAGGTGAGTACTTGGCCAGGATGCTAG 1260 TTAAATACCCTGAGATCATTAATTCAAACCAAGTGAAGCGAGTTCCTGGTCAAGGCTCAT 1320 CTGAAGATGACCTGCAGGAAGAGGAACAAATTGAGCAGGCCATCAAAGAGCATTTGAATC 1380 25 AAGGCAGCTCTCAGGAGACTGACAAGCTGGCCCCGGTGAGCAAAAGGTTCCCTGTGGGGC 1440 CCCCGAAGAATGATGATACCCCAAATAGGCAGTACTGGGATGAAGATCTGTTAATGAAAG 1500 TGCTGGAATACCTCAATCAAGAAAAGGCAGAAAAGGGAAGGGAGCATATTGCTAAGAGAG 1560 CAATGGAAAATATGTAAGCTGCTTTCATTAATTACCCTACTTTCATTCCTCCCACCCCAA 1620 GCAAATCCCAACATTTCTCTTCAGTGTGTTGACTTCTATCCTGTTAACACTGTAATATCT 1680 30 TTAAATGATGTACAGGCAGATGAAACCAGGTCACTGGGGAGTCTGCTTCATTTCCTCTGA 1740 GCTGTTATCTTGTGTATGGATATGTGTAAATGTTATGACTCCTTGATAAAAAATTTATTA 1800 TGTCCATTATTCAAGAAAGATATCTATGACTGTGTTTAATAGTATATCTAATGGCTGTGG 1860 CATTGTTGATGCTCACATATGATAAAAAAGTGTCCTATAATTCTATTGAAAGTTTTTAAT 1920 ATTTATTGAATTATTTTGTTACTGTCTGTAGCGTTTTGTGGAGTACTGGACCAAAAAAAT 1980 35 AAAGCATTATAAATATA 1997

Met Ala Glu Ala Lys Thr His Trp Leu Gly 10 Ala Ala Leu Ser Leu Ile Pro Leu Ile Phe 20 Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe 30 Gln Arg Asn Gln Leu Leu Gln Lys Glu Pro 40 Asp Leu Arq Leu Glu Asn Val Gln Lys Phe 50 Pro Ser Pro Glu Met Ile Arg Ala Leu Glu 60 Tyr Ile Glu Asn Pro Phe Lys Arg Thr Asn 70 10 Glu Ile Val Glu Glu Gln Tyr Thr Pro Gln 80 Ser Leu Ala Thr Leu Glu Ser Val Phe Gln 90 Glu Leu Gly Lys Leu Thr Gly Pro Asn Asn 100 Gln Lys Arg Glu Arg Met Asp Glu Glu Gln 110 Lys Leu Tyr Thr Asp Asp Glu Asp Asp Ile 120 15 Tyr Lys Ala Asn Asn Ile Ala Tyr Glu Asp 130 Val Val Gly Gly Glu Asp Trp Asn Pro Val 140 Glu Glu Lys Ile Glu Ser Gln Thr Gln Glu 150 Glu Val Arg Asp Ser Lys Glu Asn Ile Gly 160 Lys Asn Glu Gln Ile Asn Asp Glu Met Lys 170 20 Arg Ser Gly Gln Leu Gly Ile Gln Glu Glu 180 Asp Leu Arg Lys Glu Ser Lys Asp Gln Leu 190 Ser Asp Asp Val Ser Lys Val Ile Ala Tyr 200 Leu Lys Arg Leu Val Asn Ala Ala Gly Ser 210 Gly Arg Leu Gln Asn Gly Gln Asn Gly Glu 220 25 Arg Ala Thr Arg Leu Phe Glu Lys Pro Leu 230 Asp Ser Gln Ser Ile Tyr Gln Leu Ile Glu 240 Ile Ser Arg Asn Leu Gln Ile Pro Pro Glu 250 Asp Leu Ile Glu Met Leu Lys Thr Gly Glu 260 Lys Pro Asn Gly Ser Val Glu Pro Glu Arg 270 30 Glu Leu Asp Leu Pro Val Asp Leu Asp Asp 280 Ile Ser Glu Ala Asp Leu Asp His Pro Asp 290 Leu Phe Gln Asn Arg Met Leu Ser Lys Ser 300 Gly Tyr Pro Lys Thr Pro Gly Arg Ala Gly 310 Thr Glu Ala Leu Pro Asp Gly Leu Ser Val 320 35 Glu Asp Ile Leu Asn Leu Leu Gly Met Glu 330 Ser Ala Ala Asn Gln Lys Thr Ser Tyr Phe 340 Pro Asn Pro Tyr Asn Gln Glu Lys Val Leu 350

```
Pro Arg Leu Pro Tyr Gly Ala Gly Arg Ser 360
   Arg Ser Asn Gln Leu Pro Lys Ala Ala Trp 370
   Ile Pro His Val Glu Asn Arg Gln Met Ala 380
   Tyr Glu Asn Leu Asn Asp Lys Asp Gln Glu 390
   Leu Gly Glu Tyr Leu Ala Arg Met Leu Val 400
   Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln 410
   Val Lys Arg Val Pro Gly Gln Gly Ser Ser 420
   Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile 430
   Glu Gln Ala Ile Lys Glu His Leu Asn Gln 440
   Gly Ser Ser Gln Glu Thr Asp Lys Leu Ala 450
10
   Pro Val Ser Lys Arg Phe Pro Val Gly Pro 460
   Pro Lys Asn Asp Asp Thr Pro Asn Arg Gln 470
   Tyr Trp Asp Glu Asp Leu Leu Met Lys Val 480
   Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu 490
   Lys Gly Arg Glu His Ile Ala Lys Arg Ala 500
15
   Met Glu Asn Met
                                            504
```

			a2.	_				
			O.E.	Q ID NO: 3				
			Co-				AAAAAGAGGAAATCTTTCA TCTCTTATCCCTTTTAATTT AGCTGCTTCAGAAAGAA	
			260	O-			AAAAAGAGGAAAATCTTTCA AGCTGCTTCAGCAAAATCTTTTCA AATGATCAGAAAAGAAC TTAAGCACACAT	
			5 ACATG	GCT TATO		-4.	AAAAAGAGGAAATCTTTCA AGCTGCTTCAGAAAGATC AATGATCAGGAAAGAAC TTAAGCACATGCATTTGG	
			CCTCA	TO TGAAGC? GCTG	TCC			
			$^{CA}_{GA_{CC_T}}$	CTCTGC AAAGA	COAGCTCO			
			AGTACAT	$^{\mathrm{CA}_{GG_{\mathcal{I}''\!\mathcal{I}_{\mathrm{C}}}}}$	CCCACACACACA	TGC~		
			CCLCL	GAAA TGGAAAA	$^{A_{G}}C_{A_{G}C_{C}}$	SCATATA.		
		10	$G_{AGGA}$	GINT CLICLO	GTCCA TTCAT	TOAGCAGC	AAA	
			GAAACTIACAA	TAR GAAGAC	AAC	TCAGACTCCTG	$TC_{r}$	
			TACGCA TGACAG	TATACTCO AGAAT	TCAAGCTCA	CCCACCAAAACC	ACTOTYATO	
			$G_{G_{AC}}$	SACCAA ACCAAA	C. CAGGGA	MGA TCCTGA	GCLCLL CCLLL TOTAL	4 _
		Ą	GACA GACTO	$^{AGA}_{TG}$	CCTTGO TAA	CCC AAGAAAA	AAAAAGAGGAAATCTTTCA TCTCTTATCCCTTTTAATTT AGCTGCTTCAGAAAGAAC TTAAGCACACAGGCCTTTGG 2 CACAAATGAAATGAAATTT 30	, ,00
		15 GC	AGO: CAAAC	AACCCATATCTA	GAAACC. TACAS	LALLA SEC	TTAACCAGGGCC	150
		TGT	CTTGGCA TOAGA	ATACAGTACA	AAGGC TGAGAC	GAATCE	CACACACATO	<sub>7</sub> 80
		ACAC	TCCAAAC TCCA	GC AGGAA	$A_{GA}$ , $T_{AA}$	$r_{GAT_{GGA}} = r_{GTC}$	TraAATGA CCAATT	40
		$GT_{CT}$	$^{AA}TGGGGGGGAATT$	C-GAAGAAC	TC, MAATAGA	$\mathcal{A}_{T_{T_{GC}}}$	AAAAAAGAGGAAAATCTTTCA AGCTGCTTCAGAAAGAAC AATGATCAGGAAAGAAC TTAAGCACAATGCAATT CACAAATGAAATG	0
		$T_{GAC}$	TTTATOCAAAATO	$^{GC}CT_{AT'TC}$	COAACAAAA	$G_{TCA}$	AGCAAAA 360	,
	20	CCTT	$GC_{TC}$ $CAGC_{TC}$	GGGAA TTGAAA	CGGAAAC: CAX	CC2 AAACCCA	AAAAAAGAGGAAATCTTTCA AGCTGCTTCAGAAAGAACATCTTTCA AATGATCAGGAAAAGAAC TTAAGCACACATGCAATTTTGG 2 CACAAATGAAATGAAATTT AATGAATCAAGAGCTTTGG 360 AGCAAAAAACTTTTAAGAAATGAAACTTTAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAACTTTTAAGAAACTTTTAAGAAACTTTTAAGAAAAACTTTTAAGAAACTTTTAAGAAAACTTTTAAGAAAAACTTTTAAGAAAAACTTTTAAGAAGAAGAACACACAAAAAACTTTTAAGAAAAACTTTTAAGAAAAACTTTTAAGAAAAACTTTTAAGAAAAACTTTTAAGAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAACTTTTAAGAAAAAAAA	
		AAAn	GTTC CAAAACTC	TGAAA TGGGCCA	GGTTACT	TAN TGAGATT	AAAAAAGAGGAAATCTTTCA AGCTGCTTCAGAAAAGAATCTTTCA AATGATCAGAAAAGAAC TTCAGATCAGA	
		CCTA AGGA	TCCACCTAC	GACATCTCAA	$CA_{GGC}$	MAGACCA GA	AACC	
	2	AAA TOCAGA	COCTCTCC AGATG	ACA AGCCCCA	AATTTTTTT	$CT_{GCACC}$	AGCAAAATCTTTAAATTTTCAAATCTTTCAAATCATCAGAAAATCTTTCAGAAAATCATTTGG 2 TTAAGCACACAATGCAAATTTTCCAAAATGAAATGAAAT	
	CC	CONTRACALA	$^{CG_{G_{CT_{C}}}}$	TO TOTAL	GATE TACAGA	$G_{AA_{AC_{C}}}$	AGCTGCTTCAGAAAGAAC AATGATCAGGGCTTTTGG CACAAATGAATGAATTT AGCAAATGAAATG	
	25 TG7	TATGGT	$ACG_{TCC}$	$C^{GC}T_{ACC}$	TOAGTGO	$1_{CCCC}$	AATGATCAGAAAAGAAC TTAAGCACACATGCAATTTGG 2 TTCCAAGAATGAATTT 30 AGCAAAATGAAATTAGT 360 AGCAAAAACTTTA 480 GAAGAGGTGAG 600 CTCAGATGA 720 AGCACATGGA 720 ACGAGATGA 720 ACGAGATGA 720 ACGAGATGA 720 ACTCAGATGA 720 ACTCAGATGA 720 ACTCACATTA 780	
	$G_{T_{2}}$	GAAAAA	CTTGGCATCA ATGGCAAAATG GTTAAAAATGGTAATT TTATCAGCTAAAATG GTTCAAAAATGGTGAT GTTGACTAGATG TGCTCTCCAAGAG ACGTCGTATTTT CTGGAAGATCTAG ACGTCGTATTTT CTGGAAGATCTAG ATGCTAGTTAAT GCTCATCTGAAGA GGATCAGTTAAAT GAATCAAGGCAGA AGGCCCCCCGAAGA AGCAATGCTAGAAAA AGCAAATCTGAAAA AGCAAATCCCAAACA CTTAAATGATC	$GA_{GGAT}$	CACTTACE	CGC AGAACA	TTAAGCACCTTTTGG 2 CACAAATGAAATTAGT 360 AGCAAAAACTTTTA 480 CAAGAGCTCAGG 540 AACGCTCAGG 660 CTCAGATGA 720 ATTCTCAGGT 780 CTTAATT 780 CTTAATT	
	$A_{G_{T_{T_n}}}$	$TT_{GGCC}$	ATTTTTC ACAGAAGATCTAG ATGCTAGTTAAAT GCTCATCTGAAGA GGGCCCCCGAAGA AGCAATGGAAAAT AGCAAATCGAAAAT AGCAAATCGAAAAT ATTTTTC ATTTTTC ACAGTGCAAAAT AGCAAATCGAAAAAT ATTAAATCCCAAAC CTGTTATTC	CCAATTTTTA	"CACCTO	1TC	CTTAAT 840	
	CATTO	$CT_{GC}$	$A_{TG}$	ATCC	$A_{TC_{T'T'm_{r}}}^{GTC_{GT}}$	TOTAGACON	CTTC: 900	
	$C_{A_A}$	AGAC CAAG	GOTAGTATAT	GAAL CCACO	$^{1}CCA_{GC}$	GCTGGGA	TCC 2960	
30	$T_{GA}$	74(SO)~	~ ( '/a - ' - ' - ' - ' - ' - ' - ' - ' - ' -	71.4 X Y Y	400	1/1/2	GC2 1020	
· ·	GGA CAAGAT	* 1 ' 2	5/1 - 7/1/5	-C(1/2 VA)	~A7 ~ *(5)	n~ ~1(.)~	2080	
;	TTT						1140	
C							1500	
G'77.							1560	
35 CC7v							1320	
33 AO-							380	
Tra	TATOMAAAA	Trans TOTGA	ACAGATEGCATAT ATGCTAGATEGCATAT ATGCTAGTTAAAT GCTCATCTGAAGA GGATCAAGGCAGC AAGTGCTGGAAGA AGCAATCGGAAAAT AGCAAATCCCAAGA AGCAATCGAAAAT TTAAATCATCTTGG TCCATTATCTTGG ATTGATGCTCAC ATTGAATTATTTTT	ATAAGCT AAGAA	AAG GCAC	CGGTC 14	40	
$C_{I_{1}CI_{1}}$	TTC	TATTAT	$c_{T_{G_{TTA}}}$	ALLILCICA TECLI	TO CAGA	ACTGG 150	₹ <i>0</i>	
$^{\circ_{\mathcal{A}_{GT_{\mathcal{A}_{C'}}}}}$	'TO AAAGT'TE	$_{CT_{GT_{GC}}}$	TCCATTCTTCT	$A_{GGCAC}$ $T_{TCAGC}$	TCATTAAT	GGA 156	0	
	GACCA A	TAAT	TGTTATTCA	TATGG	GTGTTC?	Car 163		
	MAX.	AAAT, ATTI	ATT	AAAC	$CA_{GGTC}$	16P		
		· AAAGC	TIGAATTA	ATATOTA	AAATCACTGC	ATC 174		
		·	"TATAL ATTTT	CATGATAA.	ACTO TATO	GA 180		
			AGGCCCCCGAAGA AGGAATGCAAAAT AGCAAATCCCAAC TTAAATCATGTAC TCATTATTCAAG ATTGAATGATTCAAG ATTGAATGATTCAAG ATTGAATTCATCAAG ATTGAATTCATCAAG ATTGAATTATTTT	TACTGTO	GTC GTTTT	786-		
				$^{1}CT_{GT_{A}}$	ICO TCCTA	792		
					C.C.L.L.L.D.	190.		
			AGCAAATCCCAAC TTAAATGATGTAC TCATTATCTTGTG TGTTGATGTTCAAG ATTGAATGATGTAC ATTGAATTATTTTTTATAAATTATTTTT		'GTG	504		
					2,	777		
					- (	17		

	Met	Ala	Glu	Ala	Lys	Thr	His	Trp	Leu	Gly	10
	Ala	Ala	Leu	Ser	Leu	Ile	Pro	Leu	Ile	Phe	20
5	Leu	Ile	Ser	Gly	Ala	Glu	Ala	Ala	Ser	Phe	30
	Gln	Arg	Asn	Gln	Leu	Leu	Gln	Lys	Glu	Pro	40
	Asp	Leu	Arg	Leu	Glu	Asn	Val	Gln	Lys	Phe	50
	Pro	Ser	Pro	Glu	Met	Ile	Arg	Ala	Leu	Glu	60
	Tyr	Ile	Glu	Asn	Leu	Arg	Gln	Gln	Ala	His	70
10										Ser	
	Leu	Leu	Cys	Met	Lys	Arg	Ile	Pro	Gly	Ile	90
					Ala						98

	CGGGGAGGAATATGCTGTGGAGCTCCTCTGCCATATAAACAAAAAGAGGAAATCTTTCAA	60
	${\tt ACATGGCTGAAGCAAAGACCCACTGGCTTGGAGCAGCCCTGTCTCTTATCCCTTTAATTT}$	120
5	${\tt TCCTCATCTCTGGGGCTGAAGCAGCTTCATTTCAGAGAAACCAGCTGCTTCAGAAAGAA$	180
	${\tt CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG}$	240
	${\tt AGTACATAGAAAACCTCCGACAACAAGCTCATAAGGAAGAAGCAGCCCAGATTATAATC}$	300
	$\tt CCTACCAAGGTGTCTCTGTCCCCCTTCAGCAAAAAGAAAATGGCGATGAAAGCCACTTGC$	360
	$\tt CCGAGAGGGATTCACTGAGTGAAGAAGACTGGATGAGAATAATACTCGAAGCTTTGAGAC$	420
10	${\tt AGGCTGAAAATGAGCCTCAGTCTGCACCAAAAGAAAATAAGCCCTATGCCTTGAATTCAG}$	480
	AAAAGAACTTTCCAATGGACATGAGTGATGATTATGAGACACAGCAGTGGCCAGAAAGAA	540
	${\tt AGCTTAAGCACATGCAATTCCCTCCTATGTATGAAGAGAATTCCAGGGATAACCCCTTTA}$	600
	${\tt AACGCACAAATGAAATAGTGGAGGAACAATATACTCCTCAAAGCCTTGCTACATTGGAAT}$	660
	$\tt CTGTCTTCCAAGAGCTGGGGAAACTGACAGGACCAAACAACCAGAAACGTGAGAGGATGG$	720
15	${\tt ATGAGGAGCAAAAACTTTATACGGATGATGAAGATGATATCTACAAGGCTAATAACATTG}$	780
	$\tt CCTATGAAGATGTGGTCGGGGGAGAAGACTGGAACCCAGTAGAGAGAAAATAGAGAGTC$	840
	AAACCCAGGAAGAGGTGAGAGACAGCAAAGAGAAATATAGGAAAAAATGAACAAATCAACG	900
	ATGAGATGAAACGCTCAGGGCAGCTTGGCATCCAGGAAGAAGATCTTCGGAAAGAGAGTA	960
	AAGACCAACTCTCAGATGATGTCTCCAAAGTAATTGCCTATTTGAAAAGGTTAGTAAATG	1020
20	$\tt CTGCAGGAAGTGGGAAGTTACAGAATGGGCAAAATGGGGAAAGGGCCACCAGGCTTTTTG$	1080
	${\tt AGAAACCTCTTGATTCTCAGTCTATTTATCAGCTGATTGAAATCTCAAGGAATTTACAGA}$	1140
	TACCCCCAGAAGACTTAATTGAGATGCTCAAAACTGGGGAGAAGCCGAATGGATCAGTGG	1200
	AACCGGAGCGGGAGCTTGACCTTCCTGTTGACCTAGATGACATCTCAGAGGCTGACTTAG	1260
	ACCATCCAGACCTGTTCCAAAATAGGATGCTCTCCAAGAGTGGCTACCCTAAAACACCTG	1320
25	$\tt GTCGTGCTGGGACTGAGGCCCTACCAGACGGGCTCAGTGTTGAGGATATTTTAAATCTTT$	1380
	TAGGGATGGAGAGTGCAGCAAATCAGAAAACGTCGTATTTTCCCAAGCAAATCCCAACAT	1440
	${\tt TTCTCTTCAGTGTGTTGACTTCTATCCTGTTAACACTGTAATATCTTTAAATGATGTACA}$	1500
	GGCAGATGAAACCAGGTCACTGGGGAGTCTGCTTCATTTCCTCTGAGCTGTTATCTTGTG	1560
30	TATGGATATGTGTAAATGTTATGACTCCTTGATAAAAAATTTATTATGTCCATTATTCAA	1620
	GAAAGATATCTATGACTGTGTTTAATAGTATATCTAATGGCTGTGGCATTGTTGATGCTC	1680
	ACATATGATAAAAAAGTGTCCTATAATTCTATTGAAAGTTTTTAATATTTATT	1740
	TTTGTTACTGTCTGTAGCGTTTTGTGGAGTACTGGACCAAAAAAATAAAGCATTATAAAT	1800
	ATA	1803

Met Ala Glu Ala Lys Thr His Trp Leu Gly 10 Ala Ala Leu Ser Leu Ile Pro Leu Ile Phe 20 5 Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe 30 Gln Arq Asn Gln Leu Leu Gln Lys Glu Pro 40 Asp Leu Arg Leu Glu Asn Val Gln Lys Phe 50 Pro Ser Pro Glu Met Ile Arg Ala Leu Glu 60 Tyr Ile Glu Asn Leu Arq Gln Gln Ala His 70 10 Lys Glu Glu Ser Ser Pro Asp Tyr Asn Pro 80 Tyr Gln Gly Val Ser Val Pro Leu Gln Gln 90 Lys Glu Asn Gly Asp Glu Ser His Leu Pro 100 Glu Arq Asp Ser Leu Ser Glu Glu Asp Trp 110 Met Arg Ile Ile Leu Glu Ala Leu Arg Gln 120 15 Ala Glu Asn Glu Pro Gln Ser Ala Pro Lys 130 Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu 140 Lys Asn Phe Pro Met Asp Met Ser Asp Asp 150 Tyr Glu Thr Gln Gln Trp Pro Glu Arg Lys 160 Leu Lys His Met Gln Phe Pro Pro Met Tyr 170 20 Glu Glu Asn Ser Arg Asp Asn Pro Phe Lys 180 Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr 190 Thr Pro Gln Ser Leu Ala Thr Leu Glu Ser 200 Val Phe Gln Glu Leu Gly Lys Leu Thr Gly 210 Pro Asn Asn Gln Lys Arg Glu Arg Met Asp 220 25 Glu Glu Gln Lys Leu Tyr Thr Asp Asp Glu 230 Asp Asp Ile Tyr Lys Ala Asn Asn Ile Ala 240 Tyr Glu Asp Val Val Gly Glu Asp Trp 250 Asn Pro Val Glu Glu Lys Ile Glu Ser Gln 260 Thr Gln Glu Glu Val Arq Asp Ser Lys Glu 270 30 Asn Ile Gly Lys Asn Glu Gln Ile Asn Asp 280 Glu Met Lys Arg Ser Gly Gln Leu Gly Ile 290 Gln Glu Glu Asp Leu Arg Lys Glu Ser Lys 300 Asp Gln Leu Ser Asp Asp Val Ser Lys Val 310 Ile Ala Tyr Leu Lys Arg Leu Val Asn Ala 320 35 Ala Gly Ser Gly Arg Leu Gln Asn Gly Gln 330 Asn Gly Glu Arg Ala Thr Arg Leu Phe Glu 340 Lys Pro Leu Asp Ser Gln Ser Ile Tyr Gln 350

```
Leu Ile Glu Ile Ser Arg Asn Leu Gln Ile 360
Pro Pro Glu Asp Leu Ile Glu Met Leu Lys 370
Thr Gly Glu Lys Pro Asn Gly Ser Val Glu 380
Pro Glu Arg Glu Leu Asp Leu Pro Val Asp 390
Leu Asp Asp Ile Ser Glu Ala Asp Leu Asp 400
His Pro Asp Leu Phe Gln Asn Arg Met Leu 410
Ser Lys Ser Gly Tyr Pro Lys Thr Pro Gly 420
Arg Ala Gly Thr Glu Ala Leu Pro Asp Gly 430
Leu Ser Val Glu Asp Ile Leu Asn Leu Leu 440
Gly Met Glu Ser Ala Ala Asn Gln Lys Thr 450
Ser Tyr Phe Pro Lys Gln Ile Pro Thr Phe 460
Leu Phe Ser Val Leu Thr Ser Ile Leu Leu 470
Thr Leu
```